

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/650,467A
Source: 1Fw/6
Date Processed by STIC: 9/5/06

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 09/05/2006

PATENT APPLICATION: US/10/650,467A

TIME: 12:42:22

Input Set : F:\6223ndlus.txt

Output Set: N:\CRF4\09052006\J650467A.raw

3 <110> APPLICANT: Lowery, David E.
 4 Geary, Timothy G.
 5 Kubiak, Teresa M.
 6 Larsen, Martha J.
 8 <120> TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS
 10 <130> FILE REFERENCE: 30773/6223ND1US
 12 <140> CURRENT APPLICATION NUMBER: US 10/650,467A
 13 <141> CURRENT FILING DATE: 2003-08-28
 15 <160> NUMBER OF SEQ ID NOS: 243
 17 <170> SOFTWARE: PatentIn Ver. 2.0
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 1157
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Homo sapiens
 24 <220> FEATURE:
 25 <221> NAME/KEY: CDS
 26 <222> LOCATION: (1)..(1155)
 28 <220> FEATURE:
 29 <223> OTHER INFORMATION: Clone identifier: CEGPCR1a
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 34 1 5 10 15
 36 gtg att ggt gga gct gga gtt ttg gca gaa gca ggc gaa gct gaa cta 96
 37 Val Ile Gly Gly Ala Gly Val Leu Ala Glu Ala Gly Glu Ala Glu Leu
 38 20 25 30
 40 tct ggt gat gat gat ttt tat gag ctg act cct gta gaa ttg ata ata 144
 41 Ser Gly Asp Asp Asp Phe Tyr Glu Leu Thr Pro Val Glu Leu Ile Ile
 42 35 40 45
 44 tgg tgc atg ctg tat gca att ata gcc ttc atg gca gtt gtt gga aat 192
 45 Trp Cys Met Leu Tyr Ala Ile Ile Ala Phe Met Ala Val Val Gly Asn
 46 50 55 60
 48 ctt ctg gtt ctc tac ata aca ctg ttc aga tta aga gtc cgt tcc atc 240
 49 Leu Leu Val Leu Tyr Ile Thr Leu Phe Arg Leu Arg Val Arg Ser Ile
 50 65 70 75 80
 52 aca acc tac ttc att ctg aac ctc gga ttt gct gac ctc ttc act ggt 288
 53 Thr Thr Tyr Phe Ile Leu Asn Leu Gly Phe Ala Asp Leu Phe Thr Gly
 54 85 90 95
 56 att ttt gcg att ccc ttc aag ttt cag gct gct ctt ttt caa gaa tgg 336
 57 Ile Phe Ala Ile Pro Phe Lys Phe Gln Ala Ala Leu Phe Gln Glu Trp
 58 100 105 110
 60 ttc ctg ccg cga tca ctc tgc cgg ata gtt cca tac gtg gaa aca gtt 384
 61 Phe Leu Pro Arg Ser Leu Cys Arg Ile Val Pro Tyr Val Glu Thr Val

*see
p. 6*

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Input Set : E:\6223ndlus.txt

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62	115	120	125	
64	gct ctg aca gtt tca gtc ttc aca ctt gtg acg tca gca gtt cat gaa	432		
65	Ala Leu Thr Val Ser Val Phe Thr Leu Val Thr Ser Ala Val His Glu			
66	130	135	140	
68	ttc cgt aca atg ttc ttc tcg aaa tgc tca caa atg agc cca aga tct	480		
69	Phe Arg Thr Met Phe Phe Ser Lys Cys Ser Gln Met Ser Pro Arg Ser			
70	145	150	155	160
72	gca aaa cga tgt gta ctt ttg ata tgg ata atg gcg gtt ctt gtg tct	528		
73	Ala Lys Arg Cys Val Leu Leu Ile Trp Ile Met Ala Val Leu Val Ser			
74	165	170	175	
76	cta cca cat gga ttg ttc cat aat aca tac gaa ttt cca gat gac aat	576		
77	Leu Pro His Gly Leu Phe His Asn Thr Tyr Glu Phe Pro Asp Asp Asn			
78	180	185	190	
80	aat act tca att gta cag tgt ctc cca gta tat cct gat gct ggt tgg	624		
81	Asn Thr Ser Ile Val Gln Cys Leu Pro Val Tyr Pro Asp Ala Gly Trp			
82	195	200	205	
84	tgg aaa aca tac aat gtc tac ctt gtc ata atc caa tat ttt gtt cca	672		
85	Trp Lys Thr Tyr Asn Val Tyr Leu Val Ile Ile Gln Tyr Phe Val Pro			
86	210	215	220	
88	atg att att ctt gac act gcg tac aca atg att gct gtt aaa ata tgg	720		
89	Met Ile Ile Leu Asp Thr Ala Tyr Thr Met Ile Ala Val Lys Ile Trp			
90	225	230	235	240
92	tca ttg agt cag tca aga gtt gaa ctt gat gaa aca aaa atg gca acc	768		
93	Ser Leu Ser Gln Ser Arg Val Glu Leu Asp Glu Thr Lys Met Ala Thr			
94	245	250	255	
96	cag aag ctt atg cgt act ctc atc att gtc gtt gcc tgt ttc tca ttg	816		
97	Gln Lys Leu Met Arg Thr Leu Ile Ile Val Val Ala Cys Phe Ser Leu			
98	260	265	270	
100	tgt tgg ttt cca ttg gag acg tat cta ctt ttg aat gaa ttg aaa ccg	864		
101	Cys Trp Phe Pro Leu Glu Thr Tyr Leu Leu Leu Asn Glu Leu Lys Pro			
102	275	280	285	
104	gaa att aat gga tgg aaa tac atc aat ttg gtg ttc ttc ttt tca cat	912		
105	Glu Ile Asn Gly Trp Lys Tyr Ile Asn Leu Val Phe Phe Phe Ser His			
106	290	295	300	
108	tgg ctg gcg atg agc aat tct tgt ctt aat cca att att tat gga ctt	960		
109	Trp Leu Ala Met Ser Asn Ser Cys Leu Asn Pro Ile Ile Tyr Gly Leu			
110	305	310	315	320
112	tac aat aca aaa tac aac gag gaa tat cgt cgt ttg ttt cgc caa att	1008		
113	Tyr Asn Thr Lys Tyr Asn Glu Glu Tyr Arg Arg Leu Phe Arg Gln Ile			
114	325	330	335	
116	gga tgc att tgg caa cgg cag aaa agt ttg gac gat tcg atg aaa ccg	1056		
117	Gly Cys Ile Trp Gln Arg Gln Lys Ser Leu Asp Asp Ser Met Lys Pro			
118	340	345	350	
120	gag cgt cgt tgg aat tct tca aat gat tgt caa gat caa cag gaa att	1104		
121	Glu Arg Arg Trp Asn Ser Ser Asn Asp Cys Gln Asp Gln Gln Glu Ile			
122	355	360	365	
126	gat caa att gtt gat att cca cca gtt att tct aca aat aat ctt tct	1152		
127	Asp Gln Ile Val Asp Ile Pro Pro Val Ile Ser Thr Asn Asn Leu Ser			
128	370	375	380	

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Input Set : E:\6223ndlus.txt

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130 ccc tg                                     1157
131 Pro
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135 <210> SEQ ID NO: 2
136 <211> LENGTH: 385
137 <212> TYPE: PRT
138 <213> ORGANISM: Homo sapiens
140 <400> SEQUENCE: 2
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144 Val Ile Gly Gly Ala Gly Val Leu Ala Glu Ala Gly Glu Ala Glu Leu
145           20           25           30
147 Ser Gly Asp Asp Asp Phe Tyr Glu Leu Thr Pro Val Glu Leu Ile Ile
148           35           40           45
150 Trp Cys Met Leu Tyr Ala Ile Ile Ala Phe Met Ala Val Val Gly Asn
151           50           55           60
153 Leu Leu Val Leu Tyr Ile Thr Leu Phe Arg Leu Arg Val Arg Ser Ile
154           65           70           75           80
156 Thr Thr Tyr Phe Ile Leu Asn Leu Gly Phe Ala Asp Leu Phe Thr Gly
157           85           90           95
159 Ile Phe Ala Ile Pro Phe Lys Phe Gln Ala Ala Leu Phe Gln Glu Trp
160           100          105          110
162 Phe Leu Pro Arg Ser Leu Cys Arg Ile Val Pro Tyr Val Glu Thr Val
163           115          120          125
165 Ala Leu Thr Val Ser Val Phe Thr Leu Val Thr Ser Ala Val His Glu
166           130          135          140
168 Phe Arg Thr Met Phe Phe Ser Lys Cys Ser Gln Met Ser Pro Arg Ser
169 145          150          155          160
171 Ala Lys Arg Cys Val Leu Leu Ile Trp Ile Met Ala Val Leu Val Ser
172           165          170          175
174 Leu Pro His Gly Leu Phe His Asn Thr Tyr Glu Phe Pro Asp Asp Asn
175           180          185          190
177 Asn Thr Ser Ile Val Gln Cys Leu Pro Val Tyr Pro Asp Ala Gly Trp
178           195          200          205
180 Trp Lys Thr Tyr Asn Val Tyr Leu Val Ile Ile Gln Tyr Phe Val Pro
181           210          215          220
183 Met Ile Ile Leu Asp Thr Ala Tyr Thr Met Ile Ala Val Lys Ile Trp
184 225          230          235          240
186 Ser Leu Ser Gln Ser Arg Val Glu Leu Asp Glu Thr Lys Met Ala Thr
187           245          250          255
189 Gln Lys Leu Met Arg Thr Leu Ile Ile Val Val Ala Cys Phe Ser Leu
190           260          265          270
192 Cys Trp Phe Pro Leu Glu Thr Tyr Leu Leu Leu Asn Glu Leu Lys Pro
193           275          280          285
195 Glu Ile Asn Gly Trp Lys Tyr Ile Asn Leu Val Phe Phe Phe Ser His
196           290          295          300
198 Trp Leu Ala Met Ser Asn Ser Cys Leu Asn Pro Ile Ile Tyr Gly Leu
199 305          310          315          320
201 Tyr Asn Thr Lys Tyr Asn Glu Glu Tyr Arg Arg Leu Phe Arg Gln Ile

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Output Set: N:\CRF4\09052006\J650467A.raw

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202          325          330          335
204 Gly Cys Ile Trp Gln Arg Gln Lys Ser Leu Asp Asp Ser Met Lys Pro
205          340          345          350
207 Glu Arg Arg Trp Asn Ser Ser Asn Asp Cys Gln Asp Gln Gln Glu Ile
208          355          360          365
210 Asp Gln Ile Val Asp Ile Pro Pro Val Ile Ser Thr Asn Asn Leu Ser
211          370          375          380
213 Pro
214 385
217 <210> SEQ ID NO: 3
218 <211> LENGTH: 1202
219 <212> TYPE: DNA
220 <213> ORGANISM: Homo sapiens
222 <220> FEATURE:
223 <221> NAME/KEY: CDS
224 <222> LOCATION: (1)..(1200)
226 <220> FEATURE:
227 <223> OTHER INFORMATION: Clone identifier: CEGPCR1f
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232 1 5 10 15
234 gtg att ggt gga gct gga gtt ttg gca gaa gca ggc gaa gct gaa cta 96
235 Val Ile Gly Gly Ala Gly Val Leu Ala Glu Ala Gly Glu Ala Glu Leu
236 20 25 30
238 tct ggt gat gat gat ttt tat gag ctg act cct gta gaa ttg ata ata 144
239 Ser Gly Asp Asp Asp Phe Tyr Glu Leu Thr Pro Val Glu Leu Ile Ile
240 35 40 45
242 tgg tgc atg ctg tat gca att ata gcc ttc atg gca gtt gtt gga aat 192
243 Trp Cys Met Leu Tyr Ala Ile Ile Ala Phe Met Ala Val Val Gly Asn
244 50 55 60
246 ctt ctg gtt ctc tac ata aca ctg ttc aga tta aga gtc cgt tcc atc 240
247 Leu Leu Val Leu Tyr Ile Thr Leu Phe Arg Leu Arg Val Arg Ser Ile
248 65 70 75 80
251 aca acc tac ttc att ctg aac ctc gga ttt gct gac ctc ttc act ggt 288
252 Thr Thr Tyr Phe Ile Leu Asn Leu Gly Phe Ala Asp Leu Phe Thr Gly
253 85 90 95
255 att ttt gcg att ccc ttc aag ttt cag gct gct ctt ttt caa gaa tgg 336
256 Ile Phe Ala Ile Pro Phe Lys Phe Gln Ala Ala Leu Phe Gln Glu Trp
257 100 105 110
259 ttc ctg ccg cga tca ctc tgc cgg ata gtt cca tac gtg gaa aca gtt 384
260 Phe Leu Pro Arg Ser Leu Cys Arg Ile Val Pro Tyr Val Glu Thr Val
261 115 120 125
263 gct ctg aca gtt tca gtc ttc aca ctt gtg acg tca gca gtt cat gaa 432
264 Ala Leu Thr Val Ser Val Phe Thr Leu Val Thr Ser Ala Val His Glu
265 130 135 140
267 ttc cgt aca atg ttc ttc tct aaa tgc tca caa atg agc cca aga tct 480
268 Phe Arg Thr Met Phe Phe Ser Lys Cys Ser Gln Met Ser Pro Arg Ser
269 145 150 155 160

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271 gca aaa cga tgt gta ctt ttg ata tgg ata atg gcg gtt ctt gtg tct 528
272 Ala Lys Arg Cys Val Leu Leu Ile Trp Ile Met Ala Val Leu Val Ser
273      165      170      175
275 cta cca cat gga ttg ttc cat aat aca tac gaa ttt cca gat gac aat 576
276 Leu Pro His Gly Leu Phe His Asn Thr Tyr Glu Phe Pro Asp Asp Asn
277      180      185      190
279 aat act tca att gta cag tgt ctc cca gta tat cct gat gct ggt tgg 624
280 Asn Thr Ser Ile Val Gln Cys Leu Pro Val Tyr Pro Asp Ala Gly Trp
281      195      200      205
283 tgg aaa aca tac aat gtc tac ctt gtc ata atc caa tat ttt gtt cca 672
284 Trp Lys Thr Tyr Asn Val Tyr Leu Val Ile Ile Gln Tyr Phe Val Pro
285      210      215      220
287 atg att att ctt gac act gcg tac aca atg att gct gtt aaa ata tgg 720
288 Met Ile Ile Leu Asp Thr Ala Tyr Thr Met Ile Ala Val Lys Ile Trp
289 225      230      235      240
291 tca ttg agt cag tca aga gtt gaa ctt gat gaa aca aaa atg gca acc 768
292 Ser Leu Ser Gln Ser Arg Val Glu Leu Asp Glu Thr Lys Met Ala Thr
293      245      250      255
295 cag aag ata tca gtg gta tca atg gtt tca cca aac act caa tta tcg 816
296 Gln Lys Ile Ser Val Val Ser Met Val Ser Pro Asn Thr Gln Leu Ser
297      260      265      270
299 cag ctt atg cgt act ctc atc att gtc gtt gcc tgt ttc tca ttg tgt 864
300 Gln Leu Met Arg Thr Leu Ile Ile Val Val Ala Cys Phe Ser Leu Cys
301      275      280      285
303 tgg ttt cca ttg gag acg tat cta ctt ttg aat gaa ttg aaa ccg gaa 912
304 Trp Phe Pro Leu Glu Thr Tyr Leu Leu Leu Asn Glu Leu Lys Pro Glu
305      290      295      300
307 att aat gga tgg aaa tac atc aat ttg gtg ttc ttc ttt tca cat tgg 960
308 Ile Asn Gly Trp Lys Tyr Ile Asn Leu Val Phe Phe Phe Ser His Trp
309 305      310      315      320
313 ctg gcg atg agc aat tct tgt ctt aat cca att att tat gga ctt tac 1008
314 Leu Ala Met Ser Asn Ser Cys Leu Asn Pro Ile Ile Tyr Gly Leu Tyr
315      325      330      335
317 aat aca aaa tac aac gag gaa tat cgt cgt ttg ttt cgc caa att gga 1056
318 Asn Thr Lys Tyr Asn Glu Glu Tyr Arg Arg Leu Phe Arg Gln Ile Gly
319      340      345      350
321 tgc att tgg caa cgg cag aaa agt ttg gac gat tcg atg aaa ccg gag 1104
322 Cys Ile Trp Gln Arg Gln Lys Ser Leu Asp Asp Ser Met Lys Pro Glu
323      355      360      365
325 cgt cgt tgg aat tct tca aat gat tgt caa gat caa cag gaa att gat 1152
326 Arg Arg Trp Asn Ser Ser Asn Asp Cys Gln Asp Gln Gln Glu Ile Asp
327      370      375      380
329 caa att gtt gat att cca cca gtt att tct aca aat aat ctt tct ccc 1200
330 Gln Ile Val Asp Ile Pro Pro Val Ile Ser Thr Asn Asn Leu Ser Pro
331 385      390      395      400
333 tg 1202
336 <210> SEQ ID NO: 4
337 <211> LENGTH: 400
338 <212> TYPE: PRT

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 09/05/2006
PATENT APPLICATION: US/10/650,467A TIME: 12:42:23

Input Set : E:\6223ndlus.txt
Output Set: N:\CRF4\09052006\J650467A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:90; Xaa Pos. 3
Seq#:95; Xaa Pos. 1
Seq#:103; Xaa Pos. 1
Seq#:118; Xaa Pos. 1
Seq#:119; Xaa Pos. 1
Seq#:160; Xaa Pos. 1
Seq#:162; Xaa Pos. 1
Seq#:164; Xaa Pos. 1

VERIFICATION SUMMARY

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Input Set : E:\6223ndlus.txt

Output Set: N:\CRF4\09052006\J650467A.raw

L:1936 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (19) SEQUENCE:
L:1944 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (20) SEQUENCE:
L:5313 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:90 after pos.:0
L:5398 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:95 after pos.:0
L:5525 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:103 after pos.:0
L:7025 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:118 after pos.:0
L:7049 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:119 after pos.:0
L:7120 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (124) SEQUENCE:
L:7204 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (130) SEQUENCE:
L:7228 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (132) SEQUENCE:
L:7253 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (134) SEQUENCE:
L:7308 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (138) SEQUENCE:
L:7333 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (140) SEQUENCE:
L:7357 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (142) SEQUENCE:
L:7381 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (144) SEQUENCE:
L:7391 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (145) SEQUENCE:
L:7400 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (146) SEQUENCE:
L:7409 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (147) SEQUENCE:
L:7418 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (148) SEQUENCE:
L:7427 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (149) SEQUENCE:
L:7642 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:160 after pos.:0
L:7685 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:162 after pos.:0
L:7728 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:164 after pos.:0
L:7790 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (168) SEQUENCE:
L:7803 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (169) SEQUENCE:
L:7815 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (170) SEQUENCE:

STATISTICS SUMMARY

DATE: 09/05/2006

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Input Set : E:\6223ndlus.txt

Output Set: N:\CRF4\09052006\J650467A.raw

Application Serial Number: US/10/650,467A

Alpha or Numeric or Xml: Numeric

Application Class:

Application File Date: 08-28-2003

Art Unit: IFW16

Software Application: PatentIN2.0

Total Number of Sequences: 243

Total Nucleotides: 40338

Total Amino Acids: 14106

Number of Errors: 0

Number of Warnings: 26

Number of Corrections: 0

MESSAGE SUMMARY

300 W: 18 ((50) Intentionally skipped Sequence)

341 W: 8 ((46) "n" or "Xaa" used)